CLAIMS

1. A method of identifying a personalized medical intervention for a non-rodent individual predisposed to or having a disorder associated with at least one polymorphic marker in at least one gene or in at least one intergenic region, comprising the steps of:

(a) fusing cells of the non-rodent individual to rodent cell recipients to form non-rodent/rodent cell hybrids;

(b) selecting for fused cell hybrids by selecting for a first selectable marker contained on a rodent chromosome and for a second selectable marker contained on a first non-rodent individual chromosome, to form a population of fused cell hybrids;

(c) detecting among the population of fused cell hybrids a subset of hybrids which are haploid for a second non-rodent individual chromosome which is not the same chromosome as the first non-rodent individual chromosome and which was not selected;

(d) analyzing said subset of hybrids to detect a polymorphic marker in the at least one gene, in a product of the gene, or in the intergenic region, wherein the gene or intergenic region resides on the second non-rodent individual chromosome; and

(e) selecting a medical intervention based on identity of the gene or intergenic region.

2. The method of claim 1 wherein the polymorphic marker is a single nucleotide polymorphism.

3. The method of claim 1 wherein the polymorphic marker is a microsatellite marker.

4. The method of claim 1 wherein the polymorphic marker is a plurality of polymorphic markers on the second non-rodent individual chromosome.

5. The method of claim 1 wherein the polymorphic marker is a mutation.

6. The method of claim 1 wherein selection of the medical intervention is based on the identity of the polymorphic marker.

7. The method of claim 1, further comprising the step of providing the medical intervention to the non-rodent individual.

8. The method of claim 1 wherein an mRNA product of the gene is analyzed in the subset of hybrids.

9. The method of claim 1 wherein a protein product of the gene is analyzed in the subset of hybrids.

10. The method of claim 1 wherein the gene is analyzed in the subset of hybrids.

11. The method of claim 1 wherein the intergenic region is analyzed in the subset of hybrids.

12. The method of claim 1 wherein the non-rodent individual is a human.

13. The method of claim 1 wherein the non-rodent individual is a dog.

14. The method of claim 1 wherein the subset of hybrids is analyzed to detect a plurality of polymorphic markers.

15. The method of claim 1 wherein the subset of hybrids is analyzed to detect polymorphic markers in at least two different genes or in at least two different intergenic regions.

16. The method of claim 1 wherein the polymorphic marker predisposes the individual to the disorder.

17. The method of claim 16 wherein the medical intervention is a prophylactic intervention.

18. The method of claim 1 wherein the polymorphic marker is causally related to the disorder.

19. The method of claim 1 wherein the polymorphic marker is associated with responsiveness to a drug and wherein the medical intervention is administration of the drug.

20. The method of claim 1 wherein the polymorphic marker is associated with resistance to a first drug useful for treating the disorder and wherein the medical intervention is administration of a second drug useful for treating the disorder.

21. A method of identifying a non-rodent individual as eligible to participate in a clinical trial to study the efficacy of a medical intervention, comprising the steps of:

(a) fusing cells of the non-rodent individual to rodent cell recipients to

form non-rodent/rodent cell hybrids;

(b) selecting for fused cell hybrids by selecting for a first selectable marker contained on a rodent chromosome and for a second selectable marker contained on a first non-rodent chromosome, to form a population of fused cell hybrids;

(c) detecting among the population of fused cell hybrids a subset of hybrids which are haploid for a second non-rodent chromosome which is not the same chromosome as the first non-rodent chromosome and which was not selected;

(d) analyzing said subset of hybrids to detect a polymorphic marker in a gene, in a product of the gene, or in an intergenic region, wherein the gene or intergenic region resides on the second non-rodent chromosome; and

(e) identifying the non-rodent individual as eligible to participate in the clinical trial based on the presence, absence, or identity of the polymorphic marker which is detected.

22. The method of claim 21 wherein the polymorphic marker is a single nucleotide polymorphism.

23. The method of claim 21 wherein the polymorphic marker is a microsatellite marker.

24. The method of claim 21 wherein the polymorphic marker is a plurality of polymorphic markers on the second non-rodent individual chromosome.

25. The method of claim 21 wherein the polymorphic marker is a mutation.

26. The method of claim 21 wherein the at least one gene encodes a protein suspected of affecting the efficacy of a potential therapeutic agent.

27. The method of claim 21 wherein the polymorphic marker predisposes the non-rodent individual to a disorder and wherein the medical intervention may be efficacious to prevent, delay onset, or reduce severity of the disorder.

28. The method of claim 21 wherein the polymorphic marker is causally related to a disorder and wherein the medical intervention may be efficacious to treat the disorder.

29. The method of claim 21 further comprising the step of testing the non-rodent individual's response to the medical intervention.

30. The method of claim 21 wherein an mRNA product of the at least one gene is analyzed in the subset of hybrids.

31. The method of claim 21 wherein a protein product of the at least one gene is analyzed in the subset of hybrids.

32. The method of claim 21 wherein the at least one gene is analyzed in the subset of hybrids.

33. The method of claim 21 wherein the at least one intergenic region is analyzed in the subset of hybrids.

34. The method of claim 21 wherein the non-rodent individual is a human.

35. The method of claim 21 wherein the non-rodent individual is a dog.

36. The method of claim 21 wherein the subset of hybrids is analyzed to detect a plurality of polymorphic markers.

37. A method of identifying a polymorphic marker as associated with a first subpopulation of non-rodent individuals, comprising the steps of:

(a) fusing cells of a plurality of non-rodent individuals to rodent cell recipients to form a plurality of non-rodent/rodent cell hybrids;

(b) selecting for fused cell hybrids by selecting for a first selectable marker contained on a rodent chromosome and for a second selectable marker contained on a first non-rodent chromosome, to form a population of fused cell hybrids;

(c) detecting among the population of fused cell hybrids a subset of hybrids which are haploid for a second non-rodent chromosome which is not the same chromosome as the first non-rodent chromosome and which was not selected;

(d) analyzing said subset of hybrids to detect a polymorphic marker in a gene, in a product of the gene, or in an intergenic region, wherein the gene or intergenic region resides on the second non-rodent chromosome; and

(e) identifying the polymorphic marker as associated with the first subpopulation if the polymorphic marker is more prevalent in the first subpopulation and if the polymorphic marker is less prevalent in a second subpopulation of non-rodent individuals.

38. The method of claim 37 wherein the polymorphic marker is a single

nucleotide polymorphism.

39. The method of claim 37 wherein the polymorphic marker is a microsatellite marker.

40. The method of claim 37 wherein the polymorphic marker is a set of polymorphic markers on the second non-rodent chromosome.

41. The method of claim 37 wherein the polymorphic marker is a mutation.

42. The method of claim 37 wherein an mRNA product of the gene is analyzed in the subset of hybrids.

43. The method of claim 37 wherein a protein product of the gene is analyzed in the subset of hybrids.

44. The method of claim 37 wherein the gene is analyzed in the subset of hybrids.

45. The method of claim 37 wherein the intergenic region is analyzed in the subset of hybrids.

46. The method of claim 37 wherein the non-rodent individuals are humans.

47. The method of claim 37 wherein the non-rodent individuals are dogs.

48. The method of claim 37 wherein the first subpopulation is a kindred.

49. The method of claim 37 wherein the subset of hybrids is analyzed to detect a plurality of polymorphic markers.

50. The method of claim 37 wherein the subset of hybrids is analyzed to detect polymorphic markers in at least two different genes or in at least two different intergenic regions.

51. The method of claim 37 wherein the non-rodent individuals in the first subpopulation have a disorder.

52. The method of claim 51 wherein the polymorphic marker predisposes the individuals to the disorder.

53. The method of claim 51 wherein the polymorphic marker is causally related to the disorder.

54. A method of identifying a diagnostic test to be performed on a non-rodent individual predisposed to or having a disorder associated with a polymorphic

marker in at least one gene or in at least one intergenic region, comprising the steps of:

(a) fusing cells of the non-rodent individual to rodent cell recipients to form non-rodent/rodent cell hybrids;

(b) selecting for fused cell hybrids by selecting for a first selectable marker contained on a rodent chromosome and for a second selectable marker contained on a first non-rodent individual chromosome, to form a population of fused cell hybrids;

(c) detecting among the population of fused cell hybrids a subset of hybrids which are haploid for a second non-rodent individual chromosome which is not the same chromosome as the first non-rodent individual chromosome and which was not selected;

(d) analyzing said subset of hybrids to detect a polymorphic marker in the at least one gene, in a product of the at least one gene, or in the at least one intergenic region, wherein the at least one gene or intergenic region resides on the second non-rodent individual chromosome; and

(e) identifying a diagnostic test based on the presence, absence, or identity of the polymorphic marker which is detected.

55. The method of claim 54 further comprising the step of performing the diagnostic test.

56. The method of claim 54 wherein the polymorphic marker is a single nucleotide polymorphism.

57. The method of claim 54 wherein the polymorphic marker is a microsatellite marker.

58. The method of claim 54 wherein the polymorphic marker is a plurality of polymorphic markers on the second non-rodent individual chromosome.

59. The method of claim 54 wherein the polymorphic marker is a mutation.

60. The method of claim 54 wherein selection of the diagnostic test is based on the detection of a particular third polymorphic marker.

61. The method of claim 54 wherein an mRNA product of the at least one gene is analyzed in the subset of hybrids.

62. The method of claim 54 wherein a protein product of the at least one gene is analyzed in the subset of hybrids.

63. The method of claim 54 wherein the gene is analyzed in the subset of hybrids.

64. The method of claim 54 wherein the intergenic region is analyzed in the subset of hybrids.

65. The method of claim 54 wherein the non-rodent individual is a human.

66. The method of claim 54 wherein the non-rodent individual is a dog.

67. The method of claim 54 wherein the subset of hybrids is analyzed to detect a plurality of polymorphic markers.

68. The method of claim 54 wherein the subset of hybrids is analyzed to detect polymorphic markers in at least two different genes or in at least two different intergenic regions.

69. The method of claim 54 wherein the polymorphic marker predisposes the individual to the disorder.

70. The method of claim 54 wherein the polymorphic marker is causally related to the disorder.

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